UniProtKB/TrEMBL entry O75807

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**O75807_HUMAN**
Primary accession number	**O75807**
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 30, May 2005

Name and origin of the protein

Protein name	**Apoptosis associated protein**
Synonym	**Protein phosphatase 1, regulatory subunit 15A**
Gene name	**Name: PPP1R15A** Synonyms: GADD34
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE.
 DOI=10.1074/jbc.272.21.13731; PubMed=9153226 [NCBI, ExPASy, EBI, Israel, Japan]
 Hollander M.C., Zhan Q., Bae I., Fornace A.J. Jr.;
 "Mammalian GADD34, an apoptosis- and DNA damage-inducible gene.";
 J. Biol. Chem. 272:13731-13737(1997).

[2] NUCLEOTIDE SEQUENCE.
 TISSUE=Brain;
 DOI=10.1073/pnas.242603899; PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.
 Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., ↔ , Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3] NUCLEOTIDE SEQUENCE.
 TISSUE=Brain;
 Strausberg R.;
 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

Sequence databases

EMBL	U83981; AAC25631.1; -; mRNA. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC003067; AAH03067.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases
ModBase   O75807.

2D gel databases
SWISS-2DPAGE   Get region on 2D PAGE.

Organism-specific gene databases
Ensembl   ENSG00000087074; Homo sapiens. [Contig view]
HGNC   HGNC:14375; PPP1R15A.
GeneCards   PPP1R15A.
GeneLynx   PPP1R15A; Homo sapiens.
GenAtlas   PPP1R15A.
HOVERGEN [Family / Alignment / Tree]

Gene expression databases
CleanEx   HGNC:14375; PPP1R15A.

Ontologies

GO

GO:0006915; Biological process: apoptosis *(traceable author statement)*.
GO:0007050; Biological process: cell cycle arrest *(traceable author statement)*.
GO:0006974; Biological process: response to DNA damage stimulus *(traceable autho statement)*.

QuickGo
view.

Family and domain databases
ProDom   [Domain structure / List of seq. sharing at least 1 domain]

Other
ProtoMap   O75807.
PRESAGE   O75807.
UniRef   View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords
None

Features
None

Sequence information
Length: **674 AA**   Molecular weight: **73478 Da**   CRC64: **B257AA17456D1403** [This is a checksum on the sequence]

```
            10         20         30         40         50         60
    MAPGQAPHQA TPWRDAHPFF LLSPVMGLLS RAWSRLRGLG PLEPWLVEAV KGAALVEAGL

            70         80         90        100        110        120
    EGEARTPLAI PHTPWGRRPE EEAEDSGGPG EDRETLGLKT SSSLPEAWGL LDDDDGMYGE

           130        140        150        160        170        180
    REATSVPRGQ GSQFADGQRA PLSPSLLIRT LQGSDKNPGE EKAEEEGVAE EEGVNKFSYP
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       190        200        210        220        230        240
    PSHRECCPAV EEEDDEEAVK KEAHRTSTSA LSPGSKPSTW VSCPGEEENQ ATEDKRTERS

       250        260        270        280        290        300
    KGARKTSVSP RSSGSDPRSW EYRSGEASEE KEEKAHKETG KGEAAPGPQS SAPAQRPQLK

       310        320        330        340        350        360
    SWWCQPSDEE EGEVKALGAA EKDGEAECPP CIPPPSAFLK AWVYWPGEDT EEEEDEEEDE

       370        380        390        400        410        420
    DSDSGSDEEE GEAEASSSTP ATGVFLKSWV YQPGEDTEEE EDEDSDTGSA EDEREAETSA

       430        440        450        460        470        480
    STPPASAFLK AWVYRPGEDT EEEEDEDVDS EDKEDDSEAA LGEAESDPHP SHPDQRAHFR

       490        500        510        520        530        540
    GWGYRPGKET EEEEAAEDWG EAEPCPFRVA IYVPGEKPPP PWAPPRLPLR LQRRLKRPET

       550        560        570        580        590        600
    PTHDPDPETP LKARKVRFSE KVTVHFLAVW AGPAQAARQG PWEQLARDRS RFARRITQAQ

       610        620        630        640        650        660
    EELSPCLTPA ARARAWARLR NPPLAPIPAL TQTLPSSSVP SSPVQTTPLS QAVATPSRSS

       670
    AAAAAALDLS GRRG
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O75807 i
FASTA
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ScanProsite, MotifScan

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